

| | | | | | | | | | | | | | | | | | | | | | |
|-------|-----|-----|-----|------|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|----|--|
| 5'UTR | | | | | | | | | | | | | | | | | | | 1/9 | | |
| -29 | GGT | CTT | TGG | TGCT | GGA | AGGA | AAC | AGG | -1+ | M | D | L | V | L | R | K | Y | L | L | 10 | |
| SIL5 | GGT | CTT | TGG | TGCT | GGA | AGGA | AAC | AGG | ATG | GAT | CTG | GTG | CTG | AGA | AAA | TAC | CTT | CTC | 30 | | |
| | H | V | A | L | M | G | V | L | L | A | V | R | T | T | E | G | P | R | 28 | | |
| | CAT | GTG | GCT | CTG | ATG | GGT | GTT | CTT | CTG | GCT | GTA | AGG | ACC | ACA | GAA | GGA | CCC | AGA | 84 | | |
| | D | R | D | W | L | G | V | S | R | Q | L | R | I | K | A | W | N | R | 46 | | |
| | GAC | AGG | GAC | TGG | CTT | GGT | GTC | TCA | AGG | CAG | CTC | AGA | ATT | AAA | GCA | TGG | AAC | AGA | 138 | | |
| | Q | L | Y | P | E | W | T | E | S | Q | G | P | D | C | W | R | G | G | 64 | | |
| | CAG | CTG | TAT | CCA | GAG | TGG | ACA | GAA | AGC | CAG | GGG | CCT | GAC | TGC | TGG | AGA | GGT | GGC | 192 | | |
| | H | I | S | L | K | V | S | N | D | G | P | T | L | I | G | A | N | A | 82 | | |
| | CAC | ATA | TCC | CTG | AAG | GTC | AGC | AAT | GAT | GGG | CCT | ACA | CTG | ATT | GGG | GCA | AAT | GCT | 246 | | |
| | S | F | S | I | A | L | H | F | P | K | S | Q | K | V | L | P | D | G | 100 | | |
| | TCC | TTC | TCT | ATT | GCC | TTG | CAC | TTT | CCT | AAA | AGC | CAA | AAG | GTG | CTG | CCA | GAT | GGG | 300 | | |
| | Q | V | I | W | A | N | N | T | I | I | N | G | S | Q | V | W | G | G | 118 | | |
| | CAG | GTC | ATC | TGG | GCC | AAC | AAC | ACC | ATC | ATC | AAT | GGG | AGC | CAG | GTG | TGG | GGA | GGA | 354 | | |
| | Q | L | V | Y | P | Q | E | P | D | D | T | C | I | F | P | D | G | E | 136 | | |
| | CAG | CTG | GTA | TAT | CCC | CAA | GAA | CCT | GAT | GAT | ACC | TGC | ATC | TTC | CCC | GAT | GGG | GAG | 408 | | |
| | P | C | P | S | G | P | L | S | Q | K | R | C | F | V | Y | V | W | K | 154 | | |
| | CCC | TGC | CCT | TCT | GGC | CCT | CTA | TCT | CAG | AAA | AGA | TGC | TTT | GTT | TAT | GTC | TGG | AAG | 462 | | |
| | T | W | D | Q | Y | W | Q | V | L | G | G | P | V | S | G | L | S | I | 172 | | |
| | ACC | TGG | GAC | CAA | TAC | TGG | CAA | GTT | CTG | GGG | GGC | CCA | GTG | TCT | GGA | CTG | AGC | ATC | 516 | | |
| | G | T | D | K | A | M | L | G | T | Y | N | M | E | V | T | V | Y | H | 190 | | |
| | GGG | ACA | GAC | AAG | GCA | ATG | CTG | GGC | ACA | TAT | AAC | ATG | GAA | GTG | ACT | GTC | TAC | CAC | 570 | | |
| | R | R | G | S | Q | S | Y | V | P | L | A | H | S | S | S | A | F | T | 208 | | |
| | CGC | CGG | GGG | TCC | CAG | AGC | TAT | GTG | CCC | CTC | GCT | CAC | TCC | AGT | TCA | GCC | TTC | ACC | 624 | | |
| | I | T | D | Q | V | P | F | S | V | S | V | S | Q | L | Q | A | L | D | 226 | | |
| | ATT | ACT | GAC | CAG | GTG | CCC | TTC | TCT | GTG | AGT | GTG | TCT | CAG | CTG | CAG | GCC | TTG | GAT | 678 | | |
| | G | R | N | K | R | F | L | R | K | Q | P | L | T | F | A | L | Q | L | 244 | | |
| | GGA | AGG | AAC | AAG | CGC | TTC | CTG | AGA | AAG | CAG | CCT | CTG | ACC | TTT | GCC | CTC | CAG | CTC | 732 | | |
| | H | D | P | S | G | Y | L | A | G | A | D | L | S | Y | T | W | D | F | 262 | | |
| | CAT | GAT | CCC | AGT | GGC | TAT | TTG | GCT | GGG | GCT | GAC | CTT | TCC | TAC | ACC | TGG | GAC | TTT | 786 | | |
| | G | D | S | T | G | T | L | I | S | R | A | L | T | V | T | H | T | Y | 280 | | |
| | GGT | GAC | AGT | ACA | GGG | ACC | CTG | ATC | TCT | CGG | GCA | CTC | ACG | GTC | ACT | CAC | ACT | TAC | 840 | | |
| | L | E | S | G | P | V | T | A | Q | V | V | L | Q | A | A | I | P | L | 298 | | |
| | CTA | GAG | TCT | GGC | CCA | GTC | ACT | GCA | CAG | GTG | GTG | CTG | CAG | GCT | GCC | ATT | CCT | CTC | 894 | | |
| | T | S | C | G | S | S | P | V | P | G | T | T | D | R | H | V | T | T | 316 | | |
| | ACC | TCC | TGT | GGC | TCC | TCT | CCA | GTT | CCA | GGC | ACT | ACA | GAT | AGG | CAT | GTG | ACA | ACT | 948 | | |
| | A | E | A | P | G | T | T | A | G | Q | V | P | T | T | E | V | M | G | 334 | | |
| | GCA | GAG | GCT | CCT | GGA | ACC | ACA | GCT | GGC | CAA | GTG | CCT | ACT | ACA | GAA | GTC | ATG | GGC | 1002 | | |
| | T | T | P | G | Q | V | P | T | A | E | A | P | G | T | T | V | G | W | 352 | | |
| | ACC | ACA | CCT | GGC | CAG | GTG | CCA | ACT | GCA | GAG | GCC | CCT | GGC | ACC | ACA | GTT | GGG | TGG | 1056 | | |
| | V | P | T | T | E | D | V | G | T | T | P | E | Q | V | A | T | S | K | 370 | | |
| | GTG | CCA | ACC | ACA | GAG | GAT | GTA | GGT | ACC | ACA | CCT | GAG | CAG | GTG | GCA | ACC | TCC | AAA | 1110 | | |
| | V | L | S | T | T | P | V | E | M | P | T | A | K | A | T | G | R | T | 388 | | |
| | GTC | TTA | AGT | ACA | ACA | CCA | GTG | GAG | ATG | CCA | ACT | GCA | AAA | GCT | ACA | GGT | AGG | ACA | 1164 | | |

Figure 1

| | | | | | | | | | | | | | | | | | | | |
|---------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---------|-----------------|-----|-----|-------------|-----|
| P | E | V | S | T | T | E | P | S | G | T | T | V | T | Q | G | T | T | 406 | |
| CCT | GAA | GTG | TCA | ACT | ACA | GAG | CCC | TCT | GGA | ACC | ACA | GTT | ACA | CAG | GGA | ACA | ACT | 1218 | |
| P | E | L | V | E | T | T | A | G | E | V | S | T | P | E | P | A | G | 424 | |
| CCA | GAG | CTG | GTG | GAG | ACC | ACA | GCT | GGA | GAG | GTG | TCC | ACT | CCT | GAG | CCT | GCG | GGT | 1272 | |
| S | N | T | S | S | F | M | P | T | E | G | T | A | G | S | L | S | P | 442 | |
| TCA | AAT | ACT | AGC | TCA | TTC | ATG | CCT | ACA | GAA | GGT | ACT | GCA | GGC | TCC | CTG | AGT | CCC | 1326 | |
| L | P | D | D | T | A | T | L | V | L | E | K | R | Q | A | P | L | D | 460 | |
| CTG | CCG | GAT | GAC | ACT | GCC | ACC | TTA | GTC | CTG | GAG | AAG | CGC | CAA | GCC | CCC | CTG | GAT | 1380 | |
| C | V | L | Y | R | Y | G | S | F | S | L | T | L | D | I | V | Q | G | 478 | |
| TGT | GTT | CTG | TAT | CGC | TAT | GGC | TCC | TTT | TCC | CTC | ACC | CTG | GAC | ATT | GTC | CAG | GGT | 1434 | |
| I | E | S | A | E | I | L | Q | A | V | S | S | S | E | G | D | A | F | 496 | |
| ATT | GAG | AGT | GCT | GAG | ATC | CTA | CAG | GCT | GTG | TCA | TCC | AGT | GAA | GGA | GAT | GCA | TTT | 1488 | |
| E | L | T | V | S | C | Q | G | G | L | P | K | E | A | C | M | D | I | 514 | |
| GAG | CTG | ACT | GTG | TCT | TGC | CAA | GGC | GGG | CTA | CCC | AAG | GAA | GCC | TGC | ATG | GAC | ATC | 1542 | |
| S | S | P | G | C | Q | L | P | A | Q | R | L | C | Q | P | V | P | P | 532 | |
| TCA | TCG | CCA | GGG | TGT | CAG | CTG | CCT | GCC | CAG | CGG | CTG | TGT | CAG | CCT | GTG | CCC | CCC | 1596 | |
| S | P | A | C | Q | L | V | L | H | Q | V | L | K | G | G | S | G | T | 550 | |
| AGC | CCA | GCC | TGC | CAG | CTG | GTT | TTG | CAC | CAG | GTA | CTG | AAG | GGT | GGC | TCA | GGG | ACC | 1650 | |
| Y | C | L | N | V | S | L | A | D | A | N | S | L | A | M | V | S | T | 568 | |
| TAC | TGC | CTC | AAT | GTG | TCT | TTG | GCT | GAT | GCC | AAT | AGC | CTG | GCG | ATG | GTC | AGC | ACC | 1704 | |
| SIL3 → | | | | | | | | | | | | | | | | | | | |
| Q | L | V | M | P | G | Q | E | A | G | L | R | Q | A | P | L | F | V | 586 | |
| CAG | CTT | GTC | ATG | CCT | GGG | CAA | GAA | GCA | GGC | CTC | AGG | CAG | GCT | CCT | CTG | TTC | GTG | 1758 | |
| G | I | L | L | V | L | T | A | L | L | L | A | S | L | I | Y | R | R | 604 | |
| GGC | ATC | TTG | CTG | GTG | CTA | ACA | GCT | TTG | TTG | CTT | GCA | TCT | CTG | ATA | TAC | AGG | CGA | 1812 | |
| R | L | M | K | Q | G | S | A | V | P | L | P | Q | L | P | H | G | R | 622 | |
| AGA | CTT | ATG | AAG | CAA | GGC | TCA | GCA | GTC | CCC | CTT | CCC | CAG | CTG | CCA | CAC | GGT | AGA | 1866 | |
| T | Q | W | L | R | L | P | W | V | F | R | S | C | P | I | G | E | S | 640 | |
| ACC | CAG | TGG | CTA | CGT | CTG | CCC | TGG | GTC | TTC | CGC | TCT | TGC | CCC | ATT | GGT | GAG | AGC | 1920 | |
| K | P | L | L | S | G | Q | Q | V | * | | | | | | | | | SIL7 | 649 |
| AAA | CCC | CTC | CTC | AGT | GGA | CAG | CAG | GTC | TGA | GTG | CTC | TTA | TGT | GAA | GTC | ATG | ATT | 1974 | |
| SIL4 → | | | | | | | | | | | | | | | | | | | |
| TAC | CCA | GGT | GGA | CAG | CAA | GGC | CTG | TCT | TTT | CTC | TGG | TCT | TCC | CTC | AGA | GAC | TAC | 2028 | |
| SIL6 → | | | | | | | | | | | | | | | | | | | |
| CAT | TGC | CTG | AAA | TAA | AGA | CTC | AGA | ACT | TG | | | | | Poly(A) | (SEQ ID NO: 12) | | | 2057 | |
| SIL9 ← | | | | | | | | | | | | | | | | | | | |
| 3'UTR | | | | | | | | | | | | | | | | | | | |

Figure 1 (suite)

SIL10

GTTGCTGGAAGGAAGAACAGGATGGATCTGGTCTGAGAAAATACCTTCTCCATGTGGCTCTGATGGGTGTTCTTCTGGC 80
TGTAAGGACCACAGAAGGTGAGTGTGGGATGTGGACATGAACAAGTGTGAATTTGGGGTTGCACACCTGCTCTGGTTTT 160
 TCTCTCCCTAAATGGAAGATATCAGTAGTGCTTCAGGTGTCTCCACCCATTGATTTAGTGAGGACATGGGCAACTGA 240
 GCTCCCTCCCCACATGAAGATTTGGGTGCATGTGTGTTCAAGGCACTTGGGACTGAACCTGAAAACAACCCCATCTACCTG 320
 GATGGGTGAGAGAACAGTATGTCTCCGTGGCCCTAATTTTGAGATGCTCTGAATAGTGAGCTGGAACATGGGTGCCAAGG 400
 TAGTAAATGAGTGGAACTCATTAGGCTTTGTCTCAGGCACTTGGGATAGGGTATTTAGGAGATAGAGAAAGATAGGA 480
 GATAGGAGAAAGGAGAAAGAGGATGTGGTATTGGATAGAAGGTAATGAGGCACCTCATCCCTCTTTGGGATGGGCATG 560
 GGTGAACACAGCCCAGGCTTTTGTCTGGGGCTGGAAGAGACAGGCAGAAGGGTCTCAGCTGAGCATCACATGAAAGGGC 640
 TCTGGGGGATTGGGGCCTCGTGACAGGAGCAAGGCGGGTGGGGTGGGGATGGTGAGAGGGTCTGGAATGTCCCGTGCTGC 720
 TCTGAGGAGGGAGGATTGGGAGTGGAGAAAGATGGGGCATCTTATGATTCTCTTGTCTTGTGGTGAGGTATTCACTGG 800
 GATAATTCTAGATCCTCCCCAAGAGAATCAACCAGGTTTCTGGTACATGTTAGAGATGGAGTGAGGATAGTCTGTGATG 880
 TGCAGAAATATCTACATTGTACCCAGTGCCCCCTTTCTCTAGATCCCTGGTCTCACAGACTTCTTGGAACTTCTCCTTG 960
 ATCTGACTTCCCTCATTCATGGTGTCAATTCAAGTCTTATTCTTTTACTATGTTGTTTATTGTTATTCTGGAAATATCCTG 1040
 TTCATATGTGTCCACCCAGGCTCTTAATATGTTGTGCTTACTTTGGATCCAGATTTTAAATCATAGAAGACATT 1120
 TTTATATAGTTCATGAAATTTTGCATGGACTGAGTTTGATAATTTTGTTTAGTGGAATTAACATTGTGTTTATTTAAGA 1200
 AAAAAAATATTTTTTTCAGAAACCTACTGAATTTGTAGGGTTTTAAATAACATGATGTCTGGGATTTGCTTTTGAAT 1280
 GCTTCAGCCAAAAACAAACGAAACAACAAAAATAAAGGATAGATAAAGCAAATGTGACAAAATGCTGATAGTTGTTGGAC 1360
 CTTGGGGAGACACATGCAGAGCCATCACATCACTTTTTTTCAGACATCTTCTTGGTCAGTTATAATCATTGTTGTTGTC 1440
 CCCACTCCCAATTTTCTACTTGCTCTAGTCCATCCTCCTCACTGCTTGCCAAAGTGATCCTTCTAAACACAAATCTGAT 1520
 CATATTCAAAAAGCTTTTGAAGGTAAGTTTATGGTATATGCCATATATCAGTACAACAAACAAATCGTCTGAGGTGC 1600
 CGTTGCCCTACAGGATAAAGTCCAACTCCTTTGCCTGGCACTCCAAGCCCCACTCTATCTTCTTGGCCTCATCTCTCAT 1680
 GATGTACATCAGCCACATTGCTAGTGTCTGCTCATGGCCTTCTGCCTAGAATGCTTTATGCCCCAGCCAACATTTTACTG 1760
 TCTTCTTCAGTCGACCAGAGTGCAATTTACCTGTTTAAATCTATCATTTTGTATACATTGTGCATGTCTATTATGGCT 1840
 CATATTAAGCAATGCCTTGGATTATAGTAATTTATGTATATGTCTATTTTCATATACTTTAACCTGAACCCCTTCAGAACC 1920
 ATTTCTTTTTCATTTCTTAAGTTCTTTGCACCTAGCCCAGTGCCTGGTACGTCGTGGGTATTCAGTAGATTAAATGCAC 2000
 TTTAAGGAATTCCTTGTGTCCATCAAGTGGCTAAGGCTCTGTGCTCCCAATGCAGGGGACCAGGGTTCAATCTCAGG 2080
 TCAGGGAAGTAGATCCACAGGTCAACAATAAGAGTTTGCAAGCCACAACCTACCTGACCTCACATGCCACAACATAATCGA 2160
 AGATCCCTCGTGCTGCAACTAAGTCTAGTGCACTTAAATATATTTTTTAAATGCACCTTTGAATGTGAGAATGAATGATG 2240
 TGTACAGACACTGTTGTCCCTGAGAAGGGAGTGAGTAATGATTTAGGGCCCTCATAGTATATCTTCTTTTATAGGAC 2320
 CCAGAGACAGGGACTGGCTTGGTGTCTCAAGGCAGCTCAGAATTAAGCATGGAACACAGCTGTATCCAGAGTGGACA 2400
 GAAAGCCAGGGGCTGACTGCTGGAGAGGTAGGAATTTGGCAATTTCCAGGGAGGATATGGTGGAATGGGTGGGGAGGG 2480
 GAACGGGGTTGAATGTACTTAGGAAGATAGGGAAGGAAAAGGCATACAGGGAGGAGAAGCCAAGGAGCTAATTAATGCAG 2560
 CTGCCCTTTTCAAGTGGCCACATATCCCTGAAGGTCAAGATGATGGGCCTACACTGATTGGGGCAAATGCTTCTCTCTC 2640
 TATTGCCTTGCACTTTCTTAAAGCCAAAAGGTGCTGCCAGATGGGCAGGTCATCTGGGCCAACAACACCATCATCAATG 2720
 GTGAGTACCTCTCCGCCTCCTTCCCAAGGTCCAGAATCCCTGGTATCCCAATGAGCTCAAGGAATCCTCCTCTCTTTT 2800
 TTTTTTTTTTTTTTACAAATTATATATGTAACACATATTTACTGCAGAAAAATTAGAAAACACAGATAAACCAAAAAGA 2880

Figure 2

AAAAAATTATAGTTCCCAAATGGGGCACAGAAGACCCAGTGGACATAGAAGTTGGATAGACTTGGATTTAAACTGGTT 2960
 ACCAGTATGTGACCC^TGGACAAGTCACTGAATTGTTTTGTTCTTCCATTC^TCCCTTATCTATAGAATGGGGATGATAACACT 3040
 TTAAAGGTTCTTGTAAGGATTAAATGTGATAATATATAAAGATTTTAGCATAATGCCTGCCCTGTGCTGTGCTTAGTA 3120
 CCTAGTTTAGACGCTTTGCAACCCCATGGACTGTAGCCCACCAGGCTCCCTCTGTCCATGTGGATTCTGCAGSCAAGAAT 3200
 ACTGGAGTGGGTCACCATGCATCCTCCAGGGGATCTTCCCAACTCAGGGATCGAACCCAGGTCTTAGCCTACAGTATTA 3280
 ATTGATGCTGTTATTTTTACTTTTATCCCACTAGCTAGAGCACATCATCCTAGACATTTTGATACATGGCCTACCAATTT 3360
 GTGTCCAGTGTAAGAATATACATGTGTGTGCTCAGTGGCTCAGTCGTGTCTGACTCTTTGCAACCCCATGGACTGTAGCC 3440
 CGCGAAAGCTCCTCTGCCCATGGGATTGCCAGCCAAGAATACTGGAGCAGGTTGCCATTTCTTCTCCAGGGGATCTTT 3520
 CAACACAGGGATTGAATCCTTGCTCCTGTGTTTCTGCAATTGGCAGGTGTATTCTTTACCACTGAGCCACCTGGGAAAC 3600
 CCCTTAAGTATATACACATAAATCTTTTATAGTTTCCATTCTCCCTTCTACCACTCCAAATAGGTTATACCAAGGAGAAT 3680
 GTATTTTGGTAGCTAGGCAGTATTCTGGAGCCCTCTCTGGGAGTCAIGTTAAAGSTTTTGGTGTACAGTGAGGAATGC 3760
 CAGGGATTGAGGGAGACTTGCTGTCTTCTTTTCAGGGAGCCAGGTGTGGGGAGGACAGCTGGTATATCCCCAAGAACCTG 3840
 ATGATACCTGCATCTTCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAAGATGCTTTGTTTATGTCTGG 3920
 AAGACCTGGGGTAAGAGTTTCCCTTCTCTGGCCTGTCACTTACACTTAAATTCACTTCTTCTACCTGATCCCTTTCTT 4000
 TTGGTCTCATCCTTAAATTCCTGTGAGTTTCCCTAATCTTCACTTCCCCATGACTCCTTCTCTTCCACAGCACCTAGTC 4080
 AACTCTATTATACTTCTTTCTGGAGCCCTGCTCCAATTATAGTCCCATCCCATGGACCCCTCTCATAAGGACTTTTTTCC 4160
 TGCCCAACATATGCAAGCTTAAACTCTCTGAAATAACCATCCTTGATACATCTCCTGACCTTCCTTCTCTGGTTCCATCT 4240
 CTAACCTGCCCCAGTCTCCTTTGACCAGTAACCCCTTCCCTACTCTTCTTTCCAAAACCTCAGACCAATACTGGCAA 4320
 GTTCTGGGGGGCCAGTGTCTGGACTGAGCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGAAGTGT 4400
 CTACCAACCGCCGGGGTCCAGAGCTATGTGCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTGGTAAGGACTGAG 4480
 GAGGGGACAAGGCCAGTTGCAGGGCAGGAGAAGGTGGGGAGGCTGGGCTGGACAGGAAGGGGAAGAGGAAATGTTGTG 4560
 TAACCTTACAGGGGCAGAACAGGAAGATGTGGGCAGAGGATGTGGGGCTTGGAGCCCGTGAAGGGCCAGGCAGCTTGG 4640
 GTTGGTTGAAAAATATGGCTGTGAAAGAAGAAGCTGACAGAAAGAAGAACTTATGGTTCTCACTTTCTCTGACTCCAATC 4720
 CCAGACCAAGGTGCCCTTCTCTGTGAGTGTCTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGCGCTTCTGAGAAAGCA 4800
 GCCTCTGACCTTTGCCCTCCAGCTCCATGATCCAGTGGCTATTTGGCTGGGGCTGACCTTTTCTTACCTGGGACTTTG 4880
 GTGACAGTACAGGGACCTGATCTCTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCACTCACTGCACAG 4960
 GTGGTGTCTGCAGGCTGCCATTCTCTCACCTCCTGTGGCTCCTCTCCAGTTCAGGCCTACAGATAGGCATGTGACAA 5040
 TGCAGAGGCTCCTGGAACCACAGCTGGCCAAAGTGCCTACTACAGAAGTCATGGGCACACACCTGGCCAGGTGCCAACTG 5120
 CAGAGGCCCTGGCACCACAGTTGGGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCC 5200
 AAAGTCTTAAGTACAACACCAAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAGTGTCAACTACAGAGCC 5280
 CTCTGGAACCACAGTTACACAGGGAACAACCTCCAGAGCTGGTGGAGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTG 5360
 CGGGTTCAAATACTAGCTCATTTCATGCTTACAGAAGGTACTGCAGGTAAAGGGGGCCACCATGAATGAGTTCATAGAGGTG 5440
 GGGCATTTGTACAGCTCTGAAGACCTGAAAGAATTGCTCAGGACCCAGATGTTACTCAATCCTTAGCTTAGCAGTGGAG 5520
 TCCCCTCAGAATCTTCACTGGTTTTAAACCCCTAAGTCCCTCTTAATGGCACAGAATAGATCCAGAGTTCAGGAAACC 5600
 AGGGTCTTCTCCTAGGCCAGGGGTAGAGAGCTTATTCTCTCTTCTGAAGAGAAGTTCAGGAAGCAGTGTGTGATCATTT 5680
 GGTGGTGGTGCTCAGTCATGTCTGACTCTTTGTGACCTCATGGACTATGGCCACCAGGCTCCTCTGTCCATAGAATTCT 5760

Figure 2 (suite 1)

CCAGGCAAGAACACTGGAGTGGGTGGCCATTTCCTTCTCCAGGGGATTTCCCTGCCCAGGGATTAAACCCGAATTGGCA 5840
 GGTGGATTCTTTACCCGAGCCACCTAGAAAGTCCCATTGTGATCATTAGATAATACTTATACCTCATTTTCTGATTAAGTG 5920
 TAAACACAGAAATCTTTCTGACACCACTTCCCACCCCTGGATTCCCATCCCAAAGTAGGTTTACCTGGAATTGTGGTAGG 6000
 AATACTAAAAAGGGAGAGTGAAGATAGTGACACTATGACTTAACACATGTCAAATGTCTGACCCAGGACCTGGCACAGTG 6080
 TAGGGTGTGATAAACATTGGGATGTCTAAATTTCTGACTCTAACCTGTGACTCTGGGGCAGTCATTCTCTTGGGCCT 6160
 TTCTTTATCTTAAAAATGAGAGTTTCCAGCTCTTGTCTGATTCTAAGCCTGGATCCAGTAGCTCTGACTCTACCTGGAA 6240
 AAATGCTTGTGGGCCTGTTTTTCTAGGTTAGTCATTGCTTTTTGACTTTGCCCTCTTTAATCCTCTCCTCCAGGCTCCCTG 6320
 AGTCCCCTGCCGGATGACACTGCCACCTTAGTCCTGGAGAAGCGCCAAGCCCCCTGGATTGTGTTCTGTATCGCTATGG 6400
 CTCCTTTTCCCTCACCCTGGACATTGTCCGTGAGTCTTGCCCTACATTGTCCGTAAGCTGGTGGAGGGAGGCGTGTGCTGC 6480
 TTAGGGTTGCCAGTGGAAAGCACACCTTGAAGGAATTACTCACCTGGACAGGAGAATACCCAGATCCCAGGGGTTTCA 6560
 TATGAAGGCAGAATGGGATTAGGGAGGCAGCCCGAGGACCTTCTGGCCATGGGCCTTGGGGGAGGATAAGTAGAGGAGT 6640
 CTCAGACTTAAAAAATCTTGCAACTTTGCAGAGGGTATTGAGAGTGTCTGAGATCCTACAGGCTGTGTCTATCCAGTGAAG 6720
 GAGATGCATTGAGCTGACTGTGTCTTGCCAAAGCGGGTGAGTGTCCACGGTTGCCCTGAGAACTCCTGGGGTGACTGC 6800
 TGTCTGTCTCTGTGTCTAGTGTCCCTTCCCAGATTCCCTGACGTAAGCTGACATCTCTCCAGGCTACCCAAGGAAG 6880
 CCTGCATGGACATCTCATCGCCAGGGTGTCTGAGTGTCCCTGCCAGCGGCTGTGTCTGAGCCTGTGCCCCCAGCCAGCCTGC 6960
 CAGCTGGTTTTGCACCAGTACTGAAGGGTGGCTCAGGGACCTACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCT 7040
 GCGGATGGTCAGACCCAGCTTGTCTGCTGGTAGGTAGTTGGACAAGAGGTAGGATGAAGACAGGGGAGATGGTAGA 7120
 GGTACCTACTAGAGGAAGCAGACACTGAATGCAGCCGTATCTGGGATTCCACCCATAGGGCAAGAAGCAGGCCTCAGGC 7200
 AGGCTCCTCTGTTCTGTGGGCATCTTGTCTGGTCTAACAGCTTTGTTGCTTGCATCTCTGATATACAGGTGAGATCCCCGC 7280
 CATCCTGCTCCCACTCCTTTACCCCTTATTACCACCACCACTCTTCTCATGGGAAGAAGAAACCACCAACCCCTTTGGG 7360
 AAAGTGTAGAGTCCAAGAAAGAGCCAGACTTGGAAGTTCAACAGGTCTAGGCTGCAGTCTTGTCTGGTGGGACCTGGGG 7440
 AAGTCCATTAACCCCTTCTGAGCCACTGAAAAGTAGGAACATAATACCTGTCTGTGGGCTGTTTTTCAGGGCTCTAGAC 7520
 AATGTGAGTAAACACCTGGTTCTGAACAAAAGTGAATAAATGATGATCTCAATGACTGTTGTTATGAATAATATCAA 7600
 CAGTGGAGAAGAACTCAGTGAAGTGTCTCCACCTGCCAGAAAGGCAAATCCCTAGGCCTGGAGGGCTGAGGTCTCTCA 7680
 AAGCAGGGAAGCCTGTAGGGTGAGAGGGAATGGTCAGAGCTTACCATAAACATAAGAGAGGATAAACCCCTGTTGGTGAG 7760
 AAGAGGAGGGAGCCAGGATCAAGACCAAGTCAACCTGGGTTATGGTTTATGCTTTTTTTTTTAGAGAAGCACAAAGAGGT 7840
 TGCCATTGACCACCACTAACCAATATCCCTGCTTTTCTCCCAATATCAGGCGAAGACTTATGAAGCAAGGCTCAGCAGTC 7920
 CCCCCTCCCACTGCCACACGGTAGAACCCAGTGGCTACGCTGCCCCTGGGTCTTCCGCTCTTGCCCCATTGGTGAGAG 8000
 CAAACCCCTCCTCAGTGGACAGCAGGTCTGAGTGTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGT 8080
 CTTTTCTCTGGTCTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG SIL9 (SEQ ID NO: 14) 8138

Figure 2 (suite 2)

| | | |
|-----------|---|-----|
| cDNA CH | GGTCTTTGGTTGCTGGAAGGAAGAACAGGATGGATCTGGTGCTGAGAAAATACCTTCTCC | 60 |
| cDNA RPE1 | ----- | |
| cDNA CH | ATGTGGCTCTGATGGGTGTTCTTCTGGCTGTAAGGACCACAGAAGGACCCAGAGACAGGG | 120 |
| cDNA RPE1 | ----- | |
| cDNA CH | ACTGGCTTGGTGTCTCAAGGCAGCTCAGAATTAAAGCATGGAACAGACAGCTGTATCCAG | 180 |
| cDNA RPE1 | ----- | |
| cDNA CH | AGTGGACAGAAAGCCAGGGGCCCTGACTGCTGGAGAGGTGGCCACATATCCCTGAAGGTCA | 240 |
| cDNA RPE1 | ----- | |
| cDNA CH | GCAATGATGGGCCTACACTGATTGGGGCAAATGCTTCCTTCTCTATTGCCCTGCACTTTC | 300 |
| cDNA RPE1 | ----- | |
| cDNA CH | CTAAAAGCCAAAAGGTGCTGCCAGATGGGCAGGTCATCTGGGCCAACAAACACCATCATCA | 360 |
| cDNA RPE1 | ----- | |
| cDNA CH | ATGGGAGCCAGGTGTGGGGAGGACAGCTGGTATATCCCCAAGAACCTGATGATACCTGCA | 420 |
| cDNA RPE1 | ----- | |
| cDNA CH | TCTTCCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAAGATGCTTTGTTT | 480 |
| cDNA RPE1 | ----- | |
| cDNA CH | ATGTCTGGAAGACCTGGGACCAATACTGGCAAGTTCTGGGGGGCCAGTGCTGGACTGA | 540 |
| cDNA RPE1 | -----CCAATACTGGCAAGTTCTGGGGGGCCAGTGCTGGACTGA | 41 |
| | ***** | |
| cDNA CH | GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGTCTACCACC | 600 |
| cDNA RPE1 | GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGTCTACCACC | 101 |
| | ***** | |
| cDNA CH | GCCGGGGTCCCAGAGCTATGTGCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTG | 660 |
| cDNA RPE1 | GCCGGGGTCCCAGAGCTATGTGCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTG | 161 |
| | ***** | |
| cDNA CH | ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGC | 720 |
| cDNA RPE1 | ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGC | 221 |
| | ***** | |
| cDNA CH | GCTTCCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATT | 780 |
| cDNA RPE1 | GCTTCCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATT | 281 |
| | ***** | |
| cDNA CH | TGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTGGTGACAGTACAGGGACCCTGATCT | 840 |
| cDNA RPE1 | TGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTGGTGACAGTACAGGGACCCTGATCT | 341 |
| | ***** | |
| cDNA CH | CTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAGGTGG | 900 |
| cDNA RPE1 | CTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAGGTGG | 401 |
| | ***** | |
| cDNA CH | TGCTGCAGGCTGCCATTCTCTCACCTCCTGTGGCTCCTCTCCAGTTCAGGCACTACAG | 960 |
| cDNA RPE1 | TGCTGCAGGCTGCCATTCTCTCACCTCCTGTGGCTCCTCTCCAGTTCAGGCACTACAG | 461 |
| | ***** | |

Figure 3

| | | |
|-----------|--|------|
| cDNA CH | ATAGGCATGTGACAACTGCAGAGGCTCCTGGAACCAAGCTGGCCAAGTGCCTACTACAG | 1020 |
| cDNA RPE1 | ATAGGCATGTGACAACTGCAGAGGCTCCTGGAACCAAGCTGGCCAAGTGCCTACTACAG | 521 |
| ***** | | |
| cDNA CH | AAGTCATGGGCACCACACCTGGCCAGGTGCCAACTGCAGAGGCCCTGGCACCACAGTTG | 1080 |
| cDNA RPE1 | AAGTCATGGGCACCACACCTGGCCAGGTGCCAACTGCAGAGGCCCTGGCACCACAGTTG | 581 |
| ***** | | |
| cDNA CH | GGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCCAAAG | 1140 |
| cDNA RPE1 | GGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCCAAAG | 641 |
| ***** | | |
| cDNA CH | TCTTAAGTACAACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAG | 1200 |
| cDNA RPE1 | TCTTAAGTACCACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAG | 701 |
| ***** | | |
| cDNA CH | TGTCAACTACAGAGCCCTCTGGAACCAAGTTACACAGGGAACAACCTCCAGAGCTGGTGG | 1260 |
| cDNA RPE1 | TGTCAACTACAGAGCCCTCTGGAACCAAGTTACACAGGGAACAACCTCCAGAGCTGGTGG | 761 |
| ***** | | |
| cDNA CH | AGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTGCGGGTTCAAATACTAGCTCATTCA | 1320 |
| cDNA RPE1 | AGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTGCGGGTTCAAATACTAGCTCATTCA | 821 |
| ***** | | |
| cDNA CH | TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCCTGCCGGATGACACTGCCACCTTAG | 1380 |
| cDNA RPE1 | TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCCTGCCGGATGACACTGCCACCTTAG | 881 |
| ***** | | |
| cDNA CH | TCCTGGAGAAGCGCCAAGCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCCC | 1440 |
| cDNA RPE1 | TCCTGGAGAAGCGCCAAGCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCCC | 941 |
| ***** | | |
| cDNA CH | TCACCCTGGACATTGTCCAGGTTATTGAGAGTGTGAGATCCTACAGGCTGTGTATCCA | 1500 |
| cDNA RPE1 | TCACCCTGGACATTGTC---AGTATTGAGAGTGTGAGATCCTACAGGCTGTGTATCCA | 998 |
| ***** | | |
| cDNA CH | GTGAAGGAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT | 1560 |
| cDNA RPE1 | GTGAAGGAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT | 1058 |
| ***** | | |
| cDNA CH | GCATGGACATCTCATCGCCAGGGTGTGAGTGCCTGCCAGCGGCTGTGTGAGCCTGTGC | 1620 |
| cDNA RPE1 | GCATGGACATCTCATCGCCAGGGTGTGAGTGCCTGCCAGCGGCTGTGTGAGCCTGTGC | 1118 |
| ***** | | |
| cDNA CH | CCCCAGCCCAGCCTGCCAGCTGGTTTTCACACAGGTACTGAAGGGTGGCTCAGGGACCT | 1680 |
| cDNA RPE1 | CCCCAGCCCAGCCTGCCAGCTGGTTTTCACACAGGTACTGAAGGGTGGCTCAGGGACCT | 1178 |
| ***** | | |
| cDNA CH | ACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCAGCTTG | 1740 |
| cDNA RPE1 | ACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCAGCTTG | 1238 |
| ***** | | |
| cDNA CH | TCATGCCTGGGCAAGAAGCAGGCCTCAGGCAGGCTCCTCTGTTCTGTTGGGCATCTTGCTGG | 1800 |
| cDNA RPE1 | TCATGCCTGGGCAAGAAGCAGGCCTCAGGCAGGCTCCTCTGTTCTGTTGGGCATCTTGCTGG | 1298 |
| ***** | | |
| cDNA CH | TGCTAACAGCTTTGTTGCTTGCATCTCTGATATACAGGCGAAGACTTATGAAGCAAGGCT | 1860 |
| cDNA RPE1 | TGCTAACAGCTTTGTTGCTTGCATCTCTGATATACAGGCGAAGACTTATGAAGCAAGGCT | 1358 |
| ***** | | |
| cDNA CH | CAGCAGTCCCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGG | 1920 |
| cDNA RPE1 | CAGAAGTCCCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGG | 1418 |
| *** ***** | | |

Figure 3 (suite 1)

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cDNA CH      TCTTCCGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGCTGAG 1980
cDNA RPE1    TCTTCCGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGCTGAG 1478
*****

cDNA CH      TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 2040
cDNA RPE1    TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 1538
*****

cDNA CH      CTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 2086 (SEQ ID NO: 15)
cDNA RPE1    CTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 1584 (SEQ ID NO: 16)
*****
```

Figure 3 (suite 2)

| | | |
|------------|---|---------------------|
| Prot. CH | MDLVLRKYLHLHVALMGVLLAVRTTEGPRDRDWLGVSRLRIKAWNRLYPEWTESQGPDC | 60 |
| Prot. RPE1 | ----- | |
| Prot. CH | WRGGHISLKVSNDGPTLIGANASFSIALHFPKSQKVLDPGQVIWANNTIINGSQVWGGQL | 120 |
| Prot. RPE1 | ----- | |
| Prot. CH | VYPQEPDDTCIFPDGEPGPSGLSQKRCFVYVWKTDQYVQVLGGPVSGLSIGTDKAMLG | 180 |
| Prot. RPE1 | -----QYVQVLGGPVSGLSIGTDKAMLG | 23 |
| | ***** | |
| Prot. CH | TYNMEVTYHRRGSQSYVPLAHSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTF | 240 |
| Prot. RPE1 | TYNMEVTYHRRGSQSYVPLAHSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTF | 83 |
| | ***** | |
| Prot. CH | ALQLHDPGSLAGADLSYTWDFGDSTGTLSRALTVTHTYLESGPVTQVVLQAAIPLTS | 300 |
| Prot. RPE1 | ALQLHDPGSLAGADLSYTWDFGDSTGTLSRALTVTHTYLESGPVTQVVLQAAIPLTS | 143 |
| | ***** | |
| Prot. CH | CGSSPVPGTDRHVTAEAPGTTAGQVPTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVG | 360 |
| Prot. RPE1 | CGSSPVPGTDRHVTAEAPGTTAGQVPTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVG | 203 |
| | ***** | |
| Prot. CH | TTPEQVATSKVLSTTPVEMPTAKATGRTPPEVSTTEPSGTTVTQGTTPELVETTAGEVSTP | 420 |
| Prot. RPE1 | TTPEQVATSKVLSTTPVEMPTAKATGRTPPEVSTTEPSGTTVTQGTTPELVETTAGEVSTP | 263 |
| | ***** | |
| Prot. CH | EPAGSNTSSFMPTEGTAGSLSPDPDDTATLVLEKRQAPLDCVLYRYGSFSLTLDIVQIE | 480 |
| Prot. RPE1 | EPAGSNTSSFMPTEGTAGSLSPDPDDTATLVLEKRQAPLDCVLYRYGSFSLTLDIV-SIE | 322 |
| | ***** | |
| Prot. CH | SAEILQAVSSSEGDAFELTVSCQGGLPKEACMDISSPGCQLPAQRLCQPVPPSPACQLVL | 540 |
| Prot. RPE1 | SAEILQAVSSSEGDAFELTVSCQGGLPKEACMDISSPGCQLPAQRLCQPVPPSPACQLVL | 382 |
| | ***** | |
| Prot. CH | HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAQRLQAPLQVGVILLVLTALLLASL | 600 |
| Prot. RPE1 | HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAQRLQAPLQVGVILLVLTALLLASL | 442 |
| | ***** | |
| Prot. CH | IYRRRLMKQGS | 649 (SEQ ID NO: 17) |
| Prot. RPE1 | IYRRRLMKQGS | 491 (SEQ ID NO: 18) |
| | ***** | |

Figure 4